



SEQUENCE LISTING

<110> Sagami Chemical Research Center, Protegene Inc.

<120> Human proteins having hydrophobic domains and DNAs encoding these proteins

<130> 661924

<140> US/10/019,151

<141> 2003-01-31

<150> JP 11-178065

<151> 1999-06-24

<160> 24

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<212> PRT

<213> Homo sapiens

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Val	Met	Pro	Pro	Gln	Phe	Lys	Lys	Asp	Leu	Asp	Ser	Tyr	Leu	Lys	Thr
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Arg	Ser	Pro	Val	Thr	Phe	Leu	Ser	Asp	Leu	Arg	Ser	Asn	Leu	Gln	Val
	50					55				60					
Ser	Asn	Glu	Pro	Gly	Asn	Arg	Tyr	Asn	Leu	Gln	Leu	Ile	Asn	Ala	Leu
65					70				75					80	
Val	Leu	Tyr	Val	Gly	Thr	Gln	Ala	Ile	Ala	His	Ile	His	Asn	Lys	Gly
				85					90					95	
Ser	Thr	Pro	Ser	Met	Ser	Thr	Ile	Thr	His	Ser	Ala	His	Met	Asp	Ile
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Phe	Gln	Asn	Leu	Ala	Val	Asp	Leu	Asp	Thr	Glu	Gly	Arg	Tyr	Leu	Phe
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	130					135					140				
Tyr	Phe	Ser	Cys	Thr	Met	Leu	Tyr	Leu	Phe	Ala	Glu	Ala	Asn	Thr	Glu
145					150				155					160	
Ala	Ile	Gln	Glu	Gln	Ile	Thr	Arg	Val	Leu	Leu	Glu	Arg	Leu	Ile	Val
		165						170					175		
Asn	Arg	Pro	His	Pro	Trp	Gly	Leu	Leu	Ile	Thr	Phe	Ile	Glu	Leu	Ile
		180					185						190		
Lys	Asn	Pro	Ala	Phe	Lys	Phe	Trp	Asn	His	Glu	Phe	Val	His	Cys	Ala
	195						200					205			
Pro	Glu	Ile	Glu	Lys	Leu	Phe	Gln	Ser	Val	Ala	Gln	Cys	Cys	Met	Gly
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Gln	Lys	Gln	Ala	Gln	Gln	Val	Met	Glu	Gly	Thr	Gly	Ala	Ser		
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<213> Homo sapiens

<400> 2

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Asp Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His
35 40 45
Tyr Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu
50 55 60
Lys Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val
65 70 75 80
Ile Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu
85 90 95
Cys Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val
100 105 110
Ser Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly
115 120 125
Ser Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln
130 135 140
Lys Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp
145 150 155 160
Tyr Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu
165 170 175
Ile Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu
180 185 190
Phe Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro
195 200 205
Pro Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro
210 215 220
Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His
225 230 235 240
Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr
245 250 255
Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile
260 265 270
Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp
275 280 285
Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn
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Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys
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<400> 3

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35 40 45
Leu Cys Glu Lys Gly Leu Ala Ala Lys Cys Phe Asp Met Pro Val Ser
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Leu Asp Gly Asp Thr Asn Thr Ser Thr Gln Glu Val Val Gln Tyr Asn

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				85					90					95	
Met	Trp	Leu	Ser	Cys	Glu	Glu	Thr	Val	Glu	Glu	Pro	Gly	Glu	Arg	Cys
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Phe	Leu	Leu	Leu	Leu	Thr	Asp	Leu	Leu	Leu	Thr	Gly	Asn	Pro	Ala	Cys
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Gly	Leu	Lys	Leu	Ser	Ala	Phe	Ala	Ala	Val	Ser	Ser	Val	Leu	Ser	Gly
				165					170					175	
Leu	Leu	Gly	Met	Val	Ala	His	Met	Met	Tyr	Ser	Gln	Val	Phe	Gln	Ala
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Thr	Val	Asn	Leu	Gly	Pro	Glu	Asp	Trp	Arg	Pro	His	Val	Trp	Asn	Tyr
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	210					215					220				
Ser	Ala	Val	Thr	Thr	Phe	Asn	Thr	Tyr	Thr	Arg	Met	Val	Leu	Glu	Phe
225					230					235					240
Lys	Cys	Lys	His	Ser	Lys	Ser	Phe	Lys	Glu	Asn	Pro	Asn	Cys	Leu	Pro
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His	His	His	Gln	Cys	Phe	Pro	Arg	Arg	Leu	Ser	Ser	Ala	Ala	Pro	Thr
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Val	Gly	Pro	Leu	Thr	Ser	Tyr	His	Gln	Tyr	His	Asn	Gln	Pro	Ile	His
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Ser	Val	Ser	Glu	Gly	Val	Asp	Phe	Tyr	Ser	Glu	Leu	Arg	Asn	Lys	Gly
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Phe	Gln	Arg	Gly	Ala	Ser	Gln	Glu	Leu	Lys	Glu	Ala	Val	Arg	Ser	Ser
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Val	Glu	Glu	Glu	Gln	Cys										
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<400> 4															
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Ala	Gly	Pro	Asp	Glu	Asp	Leu	Ser	His	Arg	Asn	Lys	Glu	Pro	Pro	Ala
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Pro	Ala	Gln	Gln	Leu	Gln	Pro	Gln	Pro	Val	Ala	Val	Gln	Gly	Pro	Glu
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Pro	Ala	Arg	Val	Glu	Lys	Ile	Phe	Thr	Pro	Ala	Ala	Pro	Val	His	Thr
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Asn	Lys	Glu	Asp	Pro	Ala	Thr	Gln	Thr	Asn	Leu	Gly	Phe	Ile	His	Ala
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Phe	Val	Ala	Ala	Ile	Ser	Val	Ile	Ile	Val	Ser	Glu	Leu	Gly	Asp	Lys
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Thr	Phe	Phe	Ile	Ala	Ala	Ile	Met	Ala	Met	Arg	Tyr	Asn	Arg	Leu	Thr
		115					120					125			
Val	Leu	Ala	Gly	Ala	Met	Leu	Ala	Leu	Gly	Leu	Met	Thr	Cys	Leu	Ser
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Val	Leu	Phe	Gly	Tyr	Ala	Thr	Thr	Val	Ile	Pro	Arg	Val	Tyr	Thr	Tyr
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Tyr	Val	Ser	Thr	Val	Leu	Phe	Ala	Ile	Phe	Gly	Ile	Arg	Met	Leu	Arg
				165					170					175	
Glu	Gly	Leu	Lys	Met	Ser	Pro	Asp	Glu	Gly	Gln	Glu	Glu	Leu	Glu	Glu
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Val	Gln	Ala	Glu	Leu	Lys	Lys	Lys	Asp	Glu	Glu	Phe	Gln	Arg	Thr	Lys
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Leu	Leu	Asn	Gly	Pro	Gly	Asp	Val	Glu	Thr	Gly	Thr	Ser	Ile	Thr	Val
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Pro	Gln	Lys	Lys	Trp	Leu	His	Phe	Ile	Ser	Pro	Ile	Phe	Val	Gln	Ala
225					230					235					240
Leu	Thr	Leu	Thr	Phe	Leu	Ala	Glu	Trp	Gly	Asp	Arg	Ser	Gln	Leu	Thr
				245					250					255	
Thr	Ile	Val	Leu	Ala	Ala	Arg	Glu	Asp	Pro	Tyr	Gly	Val	Ala	Val	Gly
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Gly	Thr	Val	Gly	His	Cys	Leu	Cys	Thr	Gly	Leu	Ala	Val	Ile	Gly	Gly
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Arg	Met	Ile	Ala	Gln	Lys	Ile	Ser	Val	Arg	Thr	Val	Thr	Ile	Ile	Gly
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Gly	Ile	Val	Phe	Leu	Ala	Phe	Ala	Phe	Ser	Ala	Leu	Phe	Ile	Ser	Pro
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Leu	His	Ile	Val	Leu	Leu	Ser	Ile	Pro	Phe	Val	Ser	Val	Pro	Val	Val
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Trp	Thr	Leu	Thr	Asn	Leu	Ile	His	Asn	Met	Gly	Met	Tyr	Ile	Phe	Leu
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His	Thr	Val	Lys	Gly	Thr	Pro	Phe	Glu	Thr	Pro	Asp	Gln	Gly	Lys	Ala
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Arg	Leu	Leu	Thr	His	Trp	Glu	Gln	Met	Asp	Tyr	Gly	Val	Gln	Phe	Thr
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Ala	Ser	Arg	Lys	Phe	Leu	Thr	Ile	Thr	Pro	Ile	Val	Leu	Tyr	Phe	Leu
			100					105					110		
Thr	Ser	Phe	Tyr	Thr	Lys	Tyr	Asp	Gln	Ile	His	Phe	Val	Leu	Asn	Thr
		115				120						125			
Val	Ser	Leu	Met	Ser	Val	Leu	Ile	Pro	Lys	Leu	Pro	Gln	Leu	His	Gly
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			20					25					30		
Leu	His	Met	Val	Leu	Leu	Ser	Ile	Pro	Phe	Phe	Ser	Ile	Pro	Val	Val

		35				40				45							
Trp	Thr	Leu	Thr	Asn	Val	Ile	His	Asn	Leu	Ala	Thr	Tyr	Val	Phe	Leu		
	50					55					60						
His	Thr	Val	Lys	Gly	Thr	Pro	Phe	Glu	Thr	Pro	Asp	Gln	Gly	Lys	Ala		
	65				70					75					80		
Arg	Leu	Leu	Thr	His	Trp	Glu	Gln	Met	Asp	Tyr	Gly	Leu	Gln	Phe	Thr		
				85					90					95			
Ser	Ser	Arg	Lys	Phe	Leu	Ser	Ile	Ser	Pro	Ile	Val	Leu	Tyr	Leu	Leu		
			100					105					110				
Ala	Ser	Phe	Tyr	Thr	Lys	Tyr	Asp	Ala	Ala	His	Phe	Leu	Ile	Asn	Thr		
		115					120					125					
Ala	Ser	Leu	Leu	Ser	Val	Leu	Leu	Pro	Lys	Leu	Pro	Gln	Phe	His	Gly		
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			20					25					30				
Tyr	Leu	Arg	Lys	Glu	Met	Thr	Gln	Asn	Ile	Tyr	Gln	Met	Ala	Thr	Phe		
		35					40					45					
Gly	Thr	Thr	Ala	Gly	Phe	Ser	Gly	Ile	Phe	Ser	Asn	Phe	Leu	Phe	Arg		
	50				55					60							
Arg	Cys	Phe	Lys	Val	Lys	His	Asp	Ala	Leu	Lys	Thr	Tyr	Ala	Ser	Leu		
	65				70					75				80			
Ala	Thr	Leu	Pro	Phe	Leu	Ser	Thr	Val	Val	Thr	Asp	Lys	Leu	Phe	Val		
				85				90					95				
Ile	Asp	Ala	Leu	Tyr	Ser	Asp	Asn	Ile	Ser	Lys	Glu	Asn	Cys	Val	Phe		
		100					105					110					
Arg	Ser	Ser	Leu	Ile	Gly	Ile	Val	Cys	Gly	Val	Phe	Tyr	Pro	Ser	Ser		
		115				120						125					
Leu	Ala	Phe	Thr	Lys	Asn	Gly	Arg	Leu	Ala	Thr	Lys	Tyr	His	Thr	Val		
	130					135					140						
Pro	Leu	Pro	Pro	Lys	Gly	Arg	Val	Leu	Ile	His	Trp	Met	Thr	Leu	Cys		
	145				150				155					160			
Gln	Thr	Gln	Met	Lys	Leu	Met	Ala	Ile	Pro	Leu	Val	Phe	Gln	Ile	Met		
			165					170					175				
Phe	Gly	Ile	Leu	Asn	Gly	Leu	Tyr	His	Tyr	Ala	Val	Phe	Glu	Glu	Thr		
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Leu	Glu	Lys	Thr	Ile	His	Glu	Glu										
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Ile	Pro	Gly	Gly	Leu	Gly	Asp	Arg	Ala	Pro	Leu	Thr	Ala	Thr	Ala	Pro		
		20					25					30					
Gln	Leu	Asp	Asp	Glu	Glu	Met	Tyr	Ser	Ala	His	Met	Pro	Ala	His	Leu		

ggcacgtgga	atagggctta	ctcaccctt	catggaggct	cgggcagcta	ttcggtatgt	960
tcaaaactcag	acacgaaaac	cagaactgca	tcaggatatg	gtggtaccag	gagacga	1017

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ggcacacaga	aggtgcccaa	gcccctgtgc	gagaaaggtc	tggcagccaa	gtgctttgac	180
atgccagtgt	ccttggaatg	agataccaac	acatccaccc	aggaggtggt	acaatacaac	240
tgggagactg	gggatgaccg	gttctccttc	cggagcttcc	ggagtggcat	gtggctatcc	300
tgtgaggaaa	ctgtggaaga	accaggggag	aggtgccgaa	gtttcattga	acttacacca	360
ccagccaaga	gagaaatcct	atggttatcc	ctgggaacgc	agatcaccta	catcggactt	420
caattcatca	gcttcctcct	gctactaaca	gacttgctac	tcactgggaa	ccctgcctgt	480
gggctcaaac	tgagcgcctt	tgtctgtgtt	tcctctgtcc	tgtcaggtct	cctggggatg	540
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tggagaccac	atgtttggaa	ttatggctgg	gccttctaca	tggcctggct	ctccttcacc	660
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tgtttccctc	ggcggtgtgc	aagtgcagcc	cccaccgctg	gtcctttgac	cagctaccac	840
cagtatcata	atcagcccat	ccactctgtc	tctgagggag	tcgacttcta	ctccgagctg	900
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caccggaaca	aagaaccgcc	ggcgccggcc	cagcagctgc	agccgcagcc	tgtggctgtg	180
cagggccccc	agccggccc	ggtcgagaaa	atatttacac	cagcagctcc	agttcatacc	240
aataaagaag	atcctgtctac	ccaaactaat	ttgggattta	tccatgcatt	tgtcgtgcc	300
atatcagtta	ttattgtatc	tgaattgggt	gataagacat	tttttatagc	agccatcatg	360
gcaatgcgct	ataaccgcct	gaccgtgctg	gctgggtgcaa	tgcttgccct	gggactaatg	420
acatgcttgt	cagttttgtt	tggctatgcc	accacagtca	tccccagggt	ctatacatat	480
tatgtttcaa	ctgtattatt	tgccattttt	ggcattagaa	tgcttcggga	aggcttaaag	540
atgagccctg	atgagggcca	agaggaactg	gaagaagttc	aagctgaatt	aaagaagaaa	600
gatgaagaat	ttcaacgaac	caaactttta	aatggaccgg	gagatgttga	aacgggtaca	660
agcataacag tacctcagaa aaagtgggtg catttttattt caccattttt tgttcaagct						720
cttacattaa cattcttagc agaatgggggt gatcgctctc aactaactac aattgtattg						780
gcagctagag aggacccta tgggtgtagcc gtgggtggaa ctgtggggca ctgcctgtgc						840
acgggatttg cagtaattgg aggaagaatg atagcacaga aaatctctgt cagaactgtg						900
acaatcatag gaggcacgtg ttttttggcg tttgcatttt ctgcactatt tataagccct						960
gattctgggt tt						972

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ccgtttgtga gtgtccctgt cgtctggacc ctacccaacc tcattcaca catgggcatg 180
tatatcttcc tgcacacggt gaaggggaca ccctttgaga ccccggaaca gggcaaggcg 240
aggctgctaa cccactggga gcagatggat tatggggctc agttcacggc ctctcggaag 300
ttcttgacca tcacacccat cgtgctgtac ttctcacca gcttctacac taagtacgac 360
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cccttcttca gcattcctgt tgtctggacc ctgaccaacg tcattccataa cctggctacg 180
tatgtcttcc ttcatacggg gaaagggaca ccctttgaga ctctgacca aggaaaggct 240
cggctactga cacactggga gcaaatggac tatgggctcc agtttacctc ttcccgcaag 300
ttctcagca tctctctat tgtgctctat ctctggcca gcttctatac caagtatgat 360
gctgcgcact tctcatcaa cacagcctca ttgctaagtg tactgctgcc gaagttgccc 420
cagttccatg ggggttcgtgt ctttggcatc aacaaatac 459

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aatatatatc aaatggcgac atttggaaca acagctggtt tctctggaat attctcaaac 180
ttctgtttca gacgctgctt caagggttaa catgatgctt tgaagacata tgcattcttg 240
gctacacttc catttttgtc tactgttgtt actgacaagc tttttgtaat tgatgctttg 300
tattcagata atataagcaa ggaaaactgt gttttcagaa gctcactgat tggcatagtt 360
tgtgtgtgtt tctatcccag ttctttggct ttactaaaa atggacgcct ggcaaccaag 420
tatcataccg ttccactgcc accaaaagga agggttttta tccattggat gacgctttgt 480
caaacacaaa tgaaattaat ggcgattcct ctagtctttc agattatggt tggaatatta 540
aatggtctat accattatgc agtatttgaa gagacacttg agaaaactat acatgaagag 600

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ctcggggaca gggcgccact cacagccaca gccccacaac tggatgatga ggagatgtac 120
tcagcccaca tgcgcgtcct cctgcgctgt gatgcctgca gagctgtggc ttaccagatg 180
tggcaaaaatc tggcaaaagg agagacaaa ctctacacct caaactctgg ggggcggcg 240
gagctgagcg agttgggtcta cacggatgtc ctggaccgga gctgctcccg gaactggcag 300
gactacggag ttcgagaagt ggaccaagtg aaacgtctca caggcccagg acttagcgag 360
gggccagagc caagcatcag cgtgatggtc acagggggcc cctggcctac caggctctcc 420
aggacatggt tgcactactt gggggagttt ggagaagacc agatctatga agcccacaa 480
caaggccgag gggctctgga ggcattgcta tgtgggggac cccagggggc ctgctcagag 540
aaggtgtcag ccacaagaga agagctc 567

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 <211> 1167
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (187)...(903)

<400> 17
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 ttcttctaaa gaaagaaaga ctgattaata aaatgtggca gctgtgctct tcaaggcatt 120
 tatagtgtat atagtttttag aaaaacagtc ccaccactta agcatagatg taatttacta 180
 ataaaa atg att ctg ctt gtg att ctt gca ttt tat ctg tgg cag gtg 228
 Met Ile Leu Leu Val Ile Leu Ala Phe Tyr Leu Trp Gln Val
 1 5 10
 gac atg ttg agt gaa att aac att gct ccc cgg att ctc acc aat ttc 276
 Asp Met Leu Ser Glu Ile Asn Ile Ala Pro Arg Ile Leu Thr Asn Phe
 15 20 25 30
 act gga gta atg cca cct cag ttc aaa aag gat ttg gat tcc tat ctt 324
 Thr Gly Val Met Pro Gln Phe Lys Lys Asp Leu Asp Ser Tyr Leu
 35 40 45
 aaa act cga tca cca gtc act ttc ctg tct gat ctg cgc agc aac cta 372
 Lys Thr Arg Ser Pro Val Thr Phe Leu Ser Asp Leu Arg Ser Asn Leu
 50 55 60
 cag gca tcc aat gaa cct ggg aat cgc tac aac ctc cag ctc atc aat 420
 Gln Val Ser Asn Glu Pro Gly Asn Arg Tyr Asn Leu Gln Leu Ile Asn
 65 70 75
 gca ctg gtg ctc tat gtc ggg act cag gcc att gcg cac atc cac aac 468
 Ala Leu Val Leu Tyr Val Gly Thr Gln Ala Ile Ala His Ile His Asn
 80 85 90
 aag ggc agc aca cct tca atg agc acc atc act cac tca gca cac atg 516
 Lys Gly Ser Thr Pro Ser Met Ser Thr Ile Thr His Ser Ala His Met
 95 100 105 110
 gat atc ttc cag aat ttg gct gtg gac ttg gac act gag ggt cgc tat 564
 Asp Ile Phe Gln Asn Leu Ala Val Asp Leu Asp Thr Glu Gly Arg Tyr
 115 120 125
 ctc ttt ttg aat gca att gca aat cag ctc cgg tac cca aat agc cac 612
 Leu Phe Leu Asn Ala Ile Ala Asn Gln Leu Arg Tyr Pro Asn Ser His
 130 135 140
 act cac tac ttc agt tgc acc atg ctg tac ctt ttt gca gag gcc aat 660
 Thr His Tyr Phe Ser Cys Thr Met Leu Tyr Leu Phe Ala Glu Ala Asn
 145 150 155
 acg gaa gcc atc caa gaa cag atc aca aga gtt ctc ttg gaa cgg ttg 708
 Thr Glu Ala Ile Gln Glu Gln Ile Thr Arg Val Leu Leu Glu Arg Leu
 160 165 170
 att gta aat agg cca cat cct tgg ggt ctt ctt att acc ttc att gag 756
 Ile Val Asn Arg Pro His Pro Trp Gly Leu Leu Ile Thr Phe Ile Glu
 175 180 185 190
 ctg att aaa aac cca gcg ttt aag ttc tgg aac cat gaa ttt gta cac 804
 Leu Ile Lys Asn Pro Ala Phe Lys Phe Trp Asn His Glu Phe Val His
 195 200 205
 tgt gcc cca gaa atc gaa aag tta ttc cag tcg gtc gca cag tgc tgc 852
 Cys Ala Pro Glu Ile Glu Lys Leu Phe Gln Ser Val Ala Gln Cys Cys
 210 215 220
 atg gga cag aag cag gcc cag caa gta atg gaa ggg aca ggt gcc agt 900
 Met Gly Gln Lys Gln Ala Gln Gln Val Met Glu Gly Thr Gly Ala Ser
 225 230 235
 tagacgaaac tgcattctctg ttgtacgtgt cagtctagag gtctcactgc accgagttca 960
 taaactgact gaagaatcct ttcagctcct cctgactttc ccagcccttt ggtttgtggg 1020

tatctgcccc aactactgtt gggatcagcc tcctgtctta tgtgggcacg ttccaaagtt 1080
 taaatgcatt tttttgactc ttggccaaaa tttagaagat gctgtgaata tcattttgaa 1140
 cttgtgtaaa tacatgaaag agaaaaac 1167

<210> 18
 <211> 1925
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (115)... (1134)

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 Met
 1
 gcc gca gcc tgc ggg ccg gga gcg gcc ggg tac tgc ttg ctc ctc ggc 165
 Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Leu Gly
 5 10 15
 ttg cat ttg ttt ctg ctg acc gcg ggc cct gcc ctg ggc tgg aac gac 213
 Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn Asp
 20 25 30
 cct gac aga atg ttg ctg cgg gat gta aaa gct ctt acc ctc cac tat 261
 Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His Tyr
 35 40 45
 gac cgc tat acc acc tcc cgc agg ctg gat ccc atc cca cag ttg aaa 309
 Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu Lys
 50 55 60 65
 tgt gtt gga ggc aca gct ggt tgt gat tct tat acc cca aaa gtc ata 357
 Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val Ile
 70 75 80
 cag tgt cag aac aaa ggc tgg gat ggg tat gat gta cag tgg gaa tgt 405
 Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu Cys
 85 90 95
 aag acg gac tta gat att gca tac aaa ttt gga aaa act gtg gtg agc 453
 Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val Ser
 100 105 110
 tgt gaa ggc tat gag tcc tct gaa gac cag tat gta cta aga ggt tct 501
 Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly Ser
 115 120 125
 tgt ggc ttg gag tat aat tta gat tat aca gaa ctt ggc ctg cag aaa 549
 Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln Lys
 130 135 140 145
 ctg aag gag tct gga aag cag cac ggc ttt gcc tct ttc tct gat tat 597
 Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp Tyr
 150 155 160
 tat tat aag tgg tcc tcg gcg gat tcc tgt aac atg agt gga ttg att 645
 Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu Ile
 165 170 175
 acc atc gtg gta ctc ctt ggg atc gcc ttt gta gtc tat aag ctg ttc 693
 Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu Phe
 180 185 190
 ctg agt gac ggg cag tat tct cct cca ccg tac tct gag tat cct cca 741
 Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro Pro
 195 200 205
 ttt tcc cac cgt tac cag aga ttc acc aac tca gca gga cct cct ccc 789
 Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro Pro
 210 215 220 225

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cca ggc ttt aag tct gag ttc aca gga cca cag aat act ggr cat ggt 837
Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His Gly
      230      235      240
gca act tct ggt ttt ggc agt gct ttt aca gga caa caa gga tat gaa 885
Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr Glu
      245      250      255
aat tca gga cca ggg ttc tgg aca ggc ttg gga act ggt gga ata cta 933
Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile Leu
      260      265      270
gga tat ttg ttt ggc agc aat aga gcg gca aca ccc ttc tca gac tcg 981
Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp Ser
      275      280      285
tgg tac tac ccg tcc tat cct ccc tcc tac cct ggc acg tgg aat agg 1029
Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn Arg
      290      295      300      305
gct tac tca ccc ctt cat gga ggc tcg ggc agc tat tcg gta tgt tca 1077
Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys Ser
      310      315      320
aac tca gac acg aaa acc aga act gca tca gga tat ggt ggt acc agg 1125
Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr Arg
      325      330      335
aga cga taaagtagaa agttggagtc aaacactgga tgcagaaatt ttggatttt 1180
Arg Arg

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tcatacacttt ctcttttagaa aaaaagtact acctgttaac aattgggaaa aggggatatt 1240
caaaagtctt gtggtgttat gtccagtgtg gctttttgta ttctattatt tgaggctaaa 1300
agttgatgtg tgacaaaata cttatgtgtt gtatgtcagt gtaacatgca gatgtatatt 1360
gcagtttttg aaagtgatca ttactgtgga atgctaaaaa tacattaatt tctaaaacct 1420
gtgatgccct aagaagcatt aagaatgaag gtgttgtagt aatagaaact aagtacagaa 1480
aatttcagtt ttagggtggt gttagctgat agttattacc tcatagagac tataatattc 1540
tatttggtat tatatttttt gatgtttgct gttcttcaaa catttaaatac aagcttttga 1600
ctaattatgc taattttgtga gttctgatca cttttgagct ctgaagcttt gaatcattca 1660
gtggtggaga tggccttctg gtaactgaat attaccttct gtaggaaaag gtggaaaata 1720
agcatctaga aggttggtgt gaatgactct gtgctggcaa aaatgcttga aacctctata 1780
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agaatcaata aaaacaaaca agggg 1925

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<210> 19
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (71)...(1051)

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gacgctgacc atg gcc aag atg gag ctc tgc aag gcc ttc tct ggc cag 109
      Met Ala Lys Met Glu Leu Ser Lys Ala Phe Ser Gly Gln
      1      5      10
cgg aca ctc cta tct gcc atc ctc agc atg cta tca ctc agc ttc tcc 157
Arg Thr Leu Leu Ser Ala Ile Leu Ser Met Leu Ser Leu Ser Phe Ser
      15      20      25
aca aca tcc ctg ctc agc aac tac tgg ttt gtg ggc aca cag aag gtg 205
[Thr Thr Ser Leu Leu Ser Asn Tyr Trp Phe Val Gly Thr Gln Lys Val
      30      35      40      45
ccc aag ccc ctg tgc gag aaa ggt ctg gca gcc aag tgc ttt gac atg 253
Pro Lys Pro Leu Cys Glu Lys Gly Leu Ala Ala Lys Cys Phe Asp Met

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				50					55				60			
cca	gtg	tcc	ctg	gat	gga	gat	acc	aac	aca	tcc	acc	cag	gag	gtg	gta	301
Pro	Val	Ser	Leu	Asp	Gly	Asp	Thr	Asn	Thr	Ser	Thr	Gln	Glu	Val	Val	
			65					70				75				
caa	tac	aac	tgg	gag	act	ggg	gat	gac	cgg	ttc	tcc	ttc	cgg	agc	ttc	349
Gln	Tyr	Asn	Trp	Glu	Thr	Gly	Asp	Asp	Arg	Phe	Ser	Phe	Arg	Ser	Phe	
		80					85					90				
cgg	agt	ggc	atg	tgg	cta	tcc	tgt	gag	gaa	act	gtg	gaa	gaa	cca	ggg	397
Arg	Ser	Gly	Met	Trp	Leu	Ser	Cys	Glu	Glu	Thr	Val	Glu	Glu	Pro	Gly	
	95					100					105					
gag	agg	tgc	cga	agt	ttc	att	gaa	ctt	aca	cca	cca	gcc	aag	aga	gaa	445
Glu	Arg	Cys	Arg	Ser	Phe	Ile	Glu	Leu	Thr	Pro	Pro	Ala	Lys	Arg	Glu	
110					115					120					125	
atc	cta	tgg	tta	tcc	ctg	gga	acg	cag	atc	acc	tac	atc	gga	ctt	caa	493
Ile	Leu	Trp	Leu	Ser	Leu	Gly	Thr	Gln	Ile	Thr	Tyr	Ile	Gly	Leu	Gln	
			130					135					140			
ttc	atc	agc	ttc	ctc	ctg	cta	cta	aca	gac	ttg	cta	ctc	act	ggg	aac	541
Phe	Ile	Ser	Phe	Leu	Leu	Leu	Leu	Thr	Asp	Leu	Leu	Leu	Thr	Gly	Asn	
			145					150					155			
cct	gcc	tgt	ggg	ctc	aaa	ctg	agc	gcc	ttt	gct	gct	gtt	tcc	tct	gtc	589
Pro	Ala	Cys	Gly	Leu	Lys	Leu	Ser	Ala	Phe	Ala	Ala	Val	Ser	Ser	Val	
		160				165						170				
ctg	tca	ggg	ctc	ctg	ggg	atg	gtg	gcc	cac	atg	atg	tat	tca	caa	gtc	637
Leu	Ser	Gly	Leu	Leu	Gly	Met	Val	Ala	His	Met	Met	Tyr	Ser	Gln	Val	
		175				180						185				
ttc	caa	gcg	act	gtc	aac	ttg	ggg	cca	gaa	gac	tgg	aga	cca	cat	gtt	685
Phe	Gln	Ala	Thr	Val	Asn	Leu	Gly	Pro	Glu	Asp	Trp	Arg	Pro	His	Val	
190					195					200					205	
tgg	aat	tat	ggc	tgg	gcc	ttc	tac	atg	gcc	tgg	ctc	tcc	ttc	acc	tgc	733
Trp	Asn	Tyr	Gly	Trp	Ala	Phe	Tyr	Met	Ala	Trp	Leu	Ser	Phe	Thr	Cys	
			210					215						220		
tgc	atg	gcg	tgc	gct	gtc	acc	acc	ttc	aac	acg	tac	acc	agg	atg	gtg	781
Cys	Met	Ala	Ser	Ala	Val	Thr	Thr	Phe	Asn	Thr	Tyr	Thr	Arg	Met	Val	
			225					230					235			
ctg	gag	ttc	aag	tgc	aag	cat	agt	aag	agc	ttc	aag	gaa	aac	ccg	aac	829
Leu	Glu	Phe	Lys	Cys	Lys	His	Ser	Lys	Ser	Phe	Lys	Glu	Asn	Pro	Asn	
		240				245						250				
tgc	cta	cca	cat	cac	cat	cag	tgt	ttc	cct	cgg	cgg	ctg	tca	agt	gca	877
Cys	Leu	Pro	His	His	His	Gln	Cys	Phe	Pro	Arg	Arg	Leu	Ser	Ser	Ala	
		255				260						265				
gcc	ccc	acc	gtg	ggg	cct	ttg	acc	agc	tac	cac	cag	tat	cat	aat	cag	925
Ala	Pro	Thr	Val	Gly	Pro	Leu	Thr	Ser	Tyr	His	Gln	Tyr	His	Asn	Gln	
270					275					280					285	
ccc	atc	cac	tct	gtc	tct	gag	gga	gtc	gac	ttc	tac	tcc	gag	ctg	cgg	973
Pro	Ile	His	Ser	Val	Ser	Glu	Gly	Val	Asp	Phe	Tyr	Ser	Glu	Leu	Arg	
			290					295						300		
aac	aag	gga	ttt	caa	aga	ggg	gcc	agc	cag	gag	ctg	aaa	gaa	gca	gtt	1021
Asn	Lys	Gly	Phe	Gln	Arg	Gly	Ala	Ser	Gln	Glu	Leu	Lys	Glu	Ala	Val	
			305					310					315			
agg	tca	tct	gta	gag	gaa	gag	cag	tgt	taggag	ttaa	gcggg	tttgg	gg			1070
Arg	Ser	Ser	Val	Glu	Glu	Glu	Gln	Cys								
		320					325									
agtagg	cttg	agccct	acct	tacac	gtctg	ctgatt	atca	acat	gtg	ctt	aagcc					1125

<210> 20

<211> 1734

<212> DNA

<213> Homo sapiens

<220>

<221> CDS
 <222> (40)...(1014)

<400> 20

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ctctttgcggc gcccggtgcgc ggccggcccg gcaggcgagg atg gcg gcc gcg gct      54
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                                     1       5
ccg gag aac ggc cgc gca tgc gcg ccc cgg ctg ctt ctg ctc ttt ctg      102
Pro Gly Asn Gly Arg Ala Ser Ala Pro Arg Leu Leu Leu Leu Phe Leu
                                     10       15       20
gtt ccg ctg ctg tgg gcc ccg gct gcg gtc cgg gcc ggc cca gat gaa      150
Val Pro Leu Leu Trp Ala Pro Ala Ala Val Arg Ala Gly Pro Asp Glu
                                     25       30       35
gac ctt agc cac cgg aac aaa gaa ccg ccg gcg ccg gcc cag cag ctg      198
Asp Leu Ser His Arg Asn Lys Glu Pro Pro Ala Pro Ala Gln Gln Leu
                                     40       45       50
cag ccg cag cct gtg gct gtg cag ggc ccc gag ccg gcc cgg gtc gag      246
Gln Pro Gln Pro Val Ala Val Gln Gly Pro Glu Pro Ala Arg Val Glu
                                     55       60       65
aaa ata ttt aca cca gca gct cca gtt cat acc aat aaa gaa gat cct      294
Lys Ile Phe Thr Pro Ala Ala Pro Val His Thr Asn Lys Glu Asp Pro
                                     70       75       80       85
gct acc caa act aat ttg gga ttt atc cat gca ttt gtc gct gcc ata      342
Ala Thr Gln Thr Asn Leu Gly Phe Ile His Ala Phe Val Ala Ala Ile
                                     90       95       100
tca gtt att att gta tct gaa ttg ggt gat aag aca ttt ttt ata gca      390
Ser Val Ile Ile Val Ser Glu Leu Gly Asp Lys Thr Phe Phe Ile Ala
                                     105       110       115
gcc atc atg gca atg cgc tat aac cgc ctg acc gtg ctg gct ggt gca      438
Ala Ile Met Ala Met Arg Tyr Asn Arg Leu Thr Val Leu Ala Gly Ala
                                     120       125       130
atg ctt gcc ttg gga cta atg aca tgc ttg tca gtt ttg ttt ggc tat      486
Met Leu Ala Leu Gly Leu Met Thr Cys Leu Ser Val Leu Phe Gly Tyr
                                     135       140       145
gcc acc aca gtc atc ccc agg gtc tat aca tac tat gtt tca act gta      534
Ala Thr Thr Val Ile Pro Arg Val Tyr Thr Tyr Val Ser Thr Val
                                     150       155       160       165
tta ttt gcc att ttt ggc att aga atg ctt cgg gaa ggc tta aag atg      582
Leu Phe Ala Ile Phe Gly Ile Arg Met Leu Arg Glu Gly Leu Lys Met
                                     170       175       180
agc cct gat gag ggt caa gag gaa ctg gaa gaa gtt caa gct gaa tta      630
Ser Pro Asp Glu Gly Gln Glu Glu Leu Glu Glu Val Gln Ala Glu Leu
                                     185       190       195
aag aag aaa gat gaa gaa ttt caa cga acc aaa ctt tta aat gga ccg      678
Lys Lys Lys Asp Glu Glu Phe Gln Arg Thr Lys Leu Leu Asn Gly Pro
                                     200       205       210
gga gat gtt gaa acg ggt aca agc ata aca gta cct cag aaa aag tgg      726
Gly Asp Val Glu Thr Gly Thr Ser Ile Thr Val Pro Gln Lys Lys Trp
                                     215       220       225
ttg cat ttt att tca ccc att ttt gtt caa gct ctt aca tta aca ttc      774
Leu His Phe Ile Ser Pro Ile Phe Val Gln Ala Leu Thr Leu Thr Phe
                                     230       235       240       245
tta gca gaa tgg ggt gat cgc tct caa cta act aca att gta ttg gca      822
Leu Ala Glu Trp Gly Asp Arg Ser Gln Leu Thr Thr Ile Val Leu Ala
                                     250       255       260
gct aga gag gac ccc tat ggt gta gcc gtg ggt gga act gtg ggg cac      870
Ala Arg Glu Asp Pro Tyr Gly Val Ala Val Gly Gly Thr Val Gly His
                                     265       270       275
tgc ctg tgc acg gga ttg gca gta att gga gga aga atg ata gca cag      918
Cys Leu Cys Thr Gly Leu Ala Val Ile Gly Gly Arg Met Ile Ala Gln

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280	285	290	
aaa atc tct gtc aga act gtg aca atc ata aga ggc atc gtt ttt ttg			966
Lys Ile Ser Val Arg Thr Val Thr Ile Ile Gly Gly Ile Val Phe Leu			
295	300	305	
gcg ttt gca ttt tct gca cta ttt ata agc cct gat tct ggt ttt			1011
Ala Phe Ala Phe Ser Ala Leu Phe Ile Ser Pro Asp Ser Gly Phe			
310	315	320	
taacgctgt ttgttcatct atatttagtt taaaataggt agtattatct ttctgtacat			1070
agtgtacatt acaactaaaa gtgatggaaa aatactgtat tttgtagcac tgattttgtg			1130
agtttgaccc attattatgt ctgagatata atcattgatt ctatttgtaa caaggagttt			1190
taaaagaaac ctgacttcta agtgtgggtt tttcttctct ccaacataat tatgttaata			1250
tggtcctcat ttttcttttg gtgcagaacc gttgtgcagt ggggtctacc atgcaatttt			1310
ctttcagcac tgaccocctt ttaaggaata caaattttct ccttcacac ttaggtgttt			1370
taagatgttt accttaaagt ttttcttggg gaaagaatga attaatcttct atttcttaaa			1430
acatttccct gagccagtaa acagtagttt aatcattggt cttttcaaaa ctaggtgttt			1490
aaaaaaagag acatatatga tattgctgtt atatcaataa catggcacia caagaactgt			1550
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tcaatatttg acaatgtgga attacaaat taaaagagaa tactatgaat gtattcatat			1670
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cagt			1734

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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (98)...(559)

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Met Asn Val Gly Thr	
1 5	
gcg cac agc gag gtg aac ccc aac acg cgg gtg atg aac agc cgt ggc	160
Ala His Ser Glu Val Asn Pro Asn Thr Arg Val Met Asn Ser Arg Gly	
10 15 20	
atc tgg ctc tcc tac gtg ctg gcc atc ggt ctc ctc cac atc gtg ctg	208
Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly Leu Leu His Ile Val Leu	
25 30 35	
ctg agc atc ccg ttt gtg agt gtc cct gtc gtc tgg acc ctc acc aac	256
Leu Ser Ile Pro Phe Val Ser Val Pro Val Val Trp Thr Leu Thr Asn	
40 45 50	
ctc att cac aac atg ggc atg tat atc ttc ctg cac acg gtg aag ggg	304
Leu Ile His Asn Met Gly Met Tyr Ile Phe Leu His Thr Val Lys Gly	
55 60 65	
aca ccc ttt gag acc ccg gac cag ggc aag gcg agg ctg cta acc cac	352
Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala Arg Leu Leu Thr His	
70 75 80 85	
tgg gag cag atg gat tat ggg gtc cag ttc acg gcc tct cgg aag ttc	400
Trp Glu Gln Met Asp Tyr Gly Val Gln Phe Thr Ala Ser Arg Lys Phe	
90 95 100	
ttg acc atc aca ccc atc gtg ctg tac ttc ctc acc agc ttc tac act	448
Leu Thr Ile Thr Pro Ile Val Leu Tyr Phe Leu Thr Ser Phe Tyr Thr	
105 110 115	
aag tac gac cag atc cat ttt gtg ctc aac acc gtg tcc ctg atg agc	496
Lys Tyr Asp Gln Ile His Phe Val Leu Asn Thr Val Ser Leu Met Ser	
120 125 130	
gtg ctt atc ccc aag ctg ccc cag ctc cac gga gtc cgg att ttt gga	544

Val Leu Ile Pro Lys Leu Pro Gln Leu His Gly Val Arg Ile Phe Gly
135 140 145
atc aat aag tac tgagagtga gccccttccc ctgcccaggg tggcagggga gggg 600
Ile Asn Lys Tyr
150
tagggtaaaa ggcattgtgt gcaacactga agacagaaaag aagaagcctc tggacactgc 660
cagagatggg gggttagcct ctggcctaata tccccccctc gcttccccca gtagccaact 720
tggagtagct tgtagtgggg ttggggtagg ccccttgggc tctgaccttt tctgaatttt 780
ttgatctttt ccttttgcct tttgaataga gactccatgg agttgggtcat ggaatgggct 840
gggctccttg gctgaacatg gaccacgcag ttgcgcacagg aggccagggg aaaaaccctt 900
gctcacttgt ttgccctcag gcagccaaaag cactttaacc cctgcatagg gagcagaggg 960
cggtagcggt tctggattgt ttcactgtga ttcttaggtt ttttcgatgc cacgcagtgt 1020

gtgctttttgt gtatggaagc aagtgtggga tgggtctttg cctttctggg tagggagctg 1080
tctaatacaa gtcccaggct tttggcagct tctctgcaac ccaccgtggg tcttggttgg 1140
gagtggggag ggtcagggtt gggaaagatg gggtagagtg tagatggctt gggtccagag 1200
gtgagggggc cagggtctgt gccatcctgg cctggtggag gttggggagc tgtaggagag 1260
ctagttagtc gagacttaga agaatggggc cacatagcag cagaggactg gtgtaaggga 1320

gggaggggta gggacagaag ctagacccaa tctccttttg gatgtgggca gggaggggaag 1380
caggcttgga ggggttaattt acccacagaa tgtgatagta ataggggagg gaggctgctg 1440
tgggtttaac tcctgggttg gctgttgggt agacagggtg ggaaaaggcc cgtgagtcac 1500
tgtaagcaca ggtccaactt ggccctgact cctgcggggg tatggggaag ctgtgacaga 1560
aacgatgggt gctgtgggtc tctgcaggcc ctcacccctt aacttctca tacagactgg 1620
cactgggcag ggcctctcat gtggcagcca catgtggcgt tgtgaggcca cccatgttg 1680
ggtctgtggt gagagtcttg taggatccct gctcaagcag cacagaggaa ggggcaagac 1740
gtggcctgta ggcactgttt cagcctgcag agaagaaagt gaggccggga gcctgagcct 1800
gggctggagc cttctccctt cccagtttg actaggggca gtgttaattt tgaaaagggtg 1860
tgggtccctg tgtcctcttc caggggtcca agggaacagg agaggtcact gggcctgttt 1920
tctccctcct gacctgcat ctcccacccc gtgtatcata gggaactttc accttaaaat 1980
ctttctaagc aaagtgtgaa taggattttt actccctttg tacagtattc tgagaaacgc 2040
aaataaaaag gcaacatgtt tctg 2064

<210> 22
<211> 570
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (28)...(489)

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Met Asn Val Gly Val Ala His Ser
1 5
gaa gta aac ccc aac acc cga gtg atg aat agc cga ggc atc tgg ctg 99
Glu Val Asn Pro Asn Thr Arg Val Met Asn Ser Arg Gly Ile Trp Leu
10 15 20
gcc tac atc atc ttg gta gga ttg ctg cat atg gtt cta ctc agc atc 147
Ala Tyr Ile Ile Leu Val Gly Leu Leu His Met Val Leu Leu Ser Ile
25 30 35 40
ccc ttc ttc agc att cct gtt gtc tgg acc ctg acc aac gtc atc cat 195
Pro Phe Phe Ser Ile Pro Val Val Trp Thr Leu Thr Asn Val Ile His
45 50 55
aac ctg gct acg tat gtc ttc ctt cat acg gtg aaa ggg aca ccc ttt 243

Asn	Leu	Ala	Thr	Tyr	Val	Phe	Leu	His	Thr	Val	Lys	Gly	Thr	Pro	Phe		
			60					65					70				
gag	act	cct	gac	caa	gga	aag	gct	cgg	cta	ctg	aca	cac	tg	gag	caa	291	
Glu	Thr	Pro	Asp	Gln	Gly	Lys	Ala	Arg	Leu	Leu	Thr	His	Trp	Glu	Gln		
			75				80					85					
atg	gac	tat	ggg	ctc	cag	ttt	acc	tct	tcc	cgc	aag	ttc	ctc	agc	atc	339	
Met	Asp	Tyr	Gly	Leu	Gln	Phe	Thr	Ser	Ser	Arg	Lys	Phe	Leu	Ser	Ile		
			90			95					100						
tct	cct	att	gtg	ctc	tat	ctc	ctg	gcc	agc	ttc	tat	acc	aag	tat	gat	387	
Ser	Pro	Ile	Val	Leu	Tyr	Leu	Leu	Ala	Ser	Phe	Tyr	Thr	Lys	Tyr	Asp		
105					110					115					120		
gct	gcg	cac	ttc	ctc	atc	aac	aca	gcc	tca	ttg	cta	agt	gta	ctg	ctg	435	
Ala	Ala	His	Phe	Leu	Ile	Asn	Thr	Ala	Ser	Leu	Leu	Ser	Val	Leu	Leu		
				125					130					135			
ccg	aag	ttg	ccc	cag	ttc	cat	ggg	gtt	cgt	gtc	ttt	ggc	atc	aac	aaa	483	
Pro	Lys	Leu	Pro	Gln	Phe	His	Gly	Val	Arg	Val	Phe	Gly	Ile	Asn	Lys		
			140					145				150					
tac	tgag	ggatggg	ttt	tg	ggacagct	ccatggg	cat	ggggaagg	ca	ctgaaacaga						540	
Tyr																	
ggactataaa	acatccttct	cttattctcc														570	

<210> 23
 <211> 1161
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (278)... (880)

<400> 23																	
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ggtgtggtgc	cggtgggaac	tgaggaagcg	ccaaggaaa	tgaaacacga	tttccaaaat	120											
gaacttaatc	tttcatgaga	aactgaggat	agagatgtca	ataagcagcc	actgtttcca	180											
cctccccacc	tgaagagcta	ggaggacaac	tacaaagagc	ctgactgcct	tctcggaatg	240											
aggagagagg	aaaacagcaa	cagtatcagt	tttcaag atg	gca gca tct atg	292												
			Met Ala Ala Ser Met														
			1	5													
cat ggt cag	ccc agt cct	tct cta gaa	gat gca aaa	ctc aga aga	cca	340											
His Gly Gln	Pro Ser Pro	Ser Leu Glu	Asp Ala Lys	Leu Arg Arg	Pro												
		10	15	20													
atg gtc ata	gaa atc ata	gaa aaa aat	ttt gac tat	ctt aga aaa	gaa	388											
Met Val Ile	Glu Ile Ile	Glu Lys Asn	Phe Asp Tyr	Leu Arg Lys	Glu												
		25	30	35													
atg aca caa	aat ata tat	caa atg gcg	aca ttt gga	aca aca gct	ggt	436											
Met Thr Gln	Asn Ile Tyr	Gln Met Ala	Thr Phe Gly	Thr Thr Ala	Gly												
		40	45	50													
ttc tct gga	ata ttc tca	aac ttc ctg	ttc aga cgc	tgc ttc aag	ggt	484											
Phe Ser Gly	Ile Phe Ser	Asn Phe Leu	Phe Arg Arg	Cys Phe Lys	Val												
		55	60	65													
aaa cat gat	gct ttg aag	aca tat gca	tca ttg gct	aca ctt cca	ttt	532											
Lys His Asp	Ala Leu Lys	Thr Tyr Ala	Ser Leu Ala	Thr Leu Pro	Phe												
		70	75	80	85												
ttg tct act	ggt gtt act	gac aag ctt	ttt gta att	gat gct ttg	tat	580											
Leu Ser Thr	Val Val Thr	Asp Lys Leu	Phe Val Ile	Asp Ala Leu	Tyr												
		90	95	100													
tca gat aat	ata agc aag	gaa aac tgt	ggt ttc aga	agc tca ctg	att	628											
Ser Asp Asn	Ile Ser Lys	Glu Asn Cys	Val Phe Arg	Ser Ser Leu	Ile												
		105	110	115													


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ggc ata gtt tgt ggt gtt ttc tat ccc agt tct ttg gct ttt act aaa 676
Gly Ile Val Cys Gly Val Phe Tyr Pro Ser Ser Leu Ala Phe Thr Lys
120 125 130
aat gga cgc ctg gca acc aag tat cat acc gtt cca ctg cca cca aaa 724
Asn Gly Arg Leu Ala Thr Lys Tyr His Thr Val Pro Leu Pro Pro Lys
135 140 145
gga agg gtt tta atc cat tgg atg acg ctt tgt caa aca caa atg aaa 772
Gly Arg Val Leu Ile His Trp Met Thr Leu Cys Gln Thr Gln Met Lys
150 155 160 165
tta atg gcg att cct cta gtc ttt cag att atg ttt gga ata tta aat 820
Leu Met Ala Ile Pro Leu Val Phe Gln Ile Met Phe Gly Ile Leu Asn
170 175 180
ggg cta tac cat tat gca gta ttt gaa gag aca ctt gag aaa act ata 868
Gly Leu Tyr His Tyr Ala Val Phe Glu Glu Thr Leu Glu Lys Thr Ile
185 190 195
cat gaa gag taacacaaaaa aatgaatggg tgctaactta gcaaaatgaa gtt 920
His Glu Glu
200
tctataaaga ggactcaggc attgctgaaa gagttaaaag taactgtgaa caaataattt 980
gttctgtgcc ttttgccctgg tatatagcaa atactcaaaa agtattcaat aattcaatca 1040

ataaatataa gtttcatctt acacgtaaga tacagggtctt atctcctgat ggtgtgtcca 1100

ttttgcctgg tatataacag ataataaata tccagtgtca ataaatgtaa caataaaagt 1160
t 1161

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<210> 24
<211> 823
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (58)...(627)

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atg agg ctg tca ctg cca ctg ctg ctg ctg ctg gga gcc tgg gcc 105
Met Arg Leu Ser Leu Pro Leu Leu Leu Leu Leu Leu Gly Ala Trp Ala
1 5 10 15
atc cca ggg ggc ctc ggg gac agg gcg cca ctc aca gcc aca gcc cca 153
Ile Pro Gly Gly Leu Gly Asp Arg Ala Pro Leu Thr Ala Thr Ala Pro
20 25 30
caa ctg gat gat gag gag atg tac tca gcc cac atg ccc gct cac ctg 201
Gln Leu Asp Asp Glu Glu Met Tyr Ser Ala His Met Pro Ala His Leu
35 40 45
cgc tgt gat gcc tgc aga gct gtg gct tac cag atg tgg caa aat ctg 249
Arg Cys Asp Ala Cys Arg Ala Val Ala Tyr Gln Met Trp Gln Asn Leu
50 55 60
gca aag gca gag acc aaa ctt cat acc tca aac tct ggg ggg cgg cgg 297
Ala Lys Ala Glu Thr Lys Leu His Thr Ser Asn Ser Gly Gly Arg Arg
65 70 75 80
gag ctg agc gag ttg gtc tac acg gat gtc ctg gac cgg agc tgc tcc 345
Glu Leu Ser Glu Leu Val Tyr Thr Asp Val Leu Asp Arg Ser Cys Ser
85 90 95
cgg aac tgg cag gac tac gga gtt cga gaa gtg gac caa gtg aaa cgt 393
Arg Asn Trp Gln Asp Tyr Gly Val Arg Glu Val Asp Gln Val Lys Arg
100 105 110
ctc aca ggc cca gga ctt agc gag ggg cca gag cca agc atc agc gtg 441
Leu Thr Gly Pro Gly Leu Ser Glu Gly Pro Glu Pro Ser Ile Ser Val

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	115		120		125	
atg gtc aca ggg ggc ccc tgg cct acc agg ctc tcc agg aca tgt ttg						489
Met Val Thr Gly Gly Pro Trp Pro Thr Arg Leu Ser Arg Thr Cys Leu						
130		135		140		
cac tac ttg ggg gag ttt gga gaa gac cag atc tat gaa gcc cac caa						537
His Tyr Leu Gly Glu Phe Gly Glu Asp Gln Ile Tyr Glu Ala His Gln						
145		150		155		160
caa ggc cga ggg gct ctg gag gca ttg cta tgt ggg gga ccc cag ggg						585
Gln Gly Arg Gly Ala Leu Glu Ala Leu Leu Cys Gly Gly Pro Gln Gly						
	165		170		175	
gcc tgc tca gag aag gtg tca gcc aca aga gaa gag ctc tagtcc						630
Ala Cys Ser Glu Lys Val Ser Ala Thr Arg Glu Glu Leu						
	180		185			
tggaactctac cctcctctga aagaagctgg ggcttgctct gacgggtctcc actcccgctct						690
gcaggcagcc aggagggcag gaagcccttg ctctgtgctg ccatacctgcc tccctcctcc						750
agcctcaggg cactcggggc tgggtgggag tcaacgcctt cccctctgga ctcaaataaa						810
accagtgac ctc						823